

SEQUENCE LISTING

<110> SIRS-Lab GmbH

5 <120> Method of enriching/separating prokaryotic DNA by means of
a protein which specifically binds DNA containing non-methylated
CpG motifs

10 <130> Pat 3696/29-PCT

<140>
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15 <160> 8

<170> PatentIn Ver. 2.1

20 <210> 1
<211> 543
<212> DNA
<213> Homo sapiens

25 <220>
<221> CDS
<222> (1)..(561)

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Gly Gly Gly Arg Lys Arg Pro Val Pro Asp Pro Asn Leu Gln Arg Arg
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35 gca ggg tca ggg aca ggg gtt ggg gcc atg ctt gct cgg ggc tct gct 96
Ala Gly Ser Gly Thr Gly Val Gly Ala Met Leu Ala Arg Gly Ser Ala
20 25 30

40 tcg ccc cac aaa tcc tct ccg cag ccc ttg gtg gcc aca ccc agc cag 144
Ser Pro His Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln
35 40 45

45 cat cac cag cag cag cag atc aaa cgg tca gcc cgc atg tgt 192
His His Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys
50 55 60

55 ggt gag tgt gag gca tgt ccg cgc act gag gac tgt ggt cac tgt gat 240
Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp
65 70 75 80

60 ttc tgt cgg gac atg aag aag ttc ggg ggc ccc aac aag atc cgg cag 288
Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln
85 90 95

70 aag tgc cgg ctg cgc cag tgc cag ctg cgg gcc cgg gaa tcg tac aag 336
Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys
100 105 110

75 tac ttc cct tcc tcg ctc tca cca gtg acg ccc tca gag tcc ctg cca 384
Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro
115 120 125

agg ccc cgc cg_g cca ctg ccc acc caa cag cag cca cag cca tca cag 432
Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln
130 135 140

5 aag tta ggg cg_c atc cgt gaa gat gag ggg gca gtg gc_g tca tca aca 480
Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr
145 150 155 160

10 gtc aag gag cct cct gag gct aca gcc aca cct gag cca ctc tca gat 528
Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp
165 170 175

15 gag gac cta cct ctg 543
Glu Asp Leu Pro Leu
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<210> 2

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<212> PRT

<213> Homo sapiens

<400> 2

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30 Ser Pro His Lys Ser Ser Pro Gln Pro Leu Val Ala Thr Pro Ser Gln 35 40 45

35 His His Gln Gln Gln Gln Gln Ile Lys Arg Ser Ala Arg Met Cys 50 55 60

Gly Glu Cys Glu Ala Cys Arg Arg Thr Glu Asp Cys Gly His Cys Asp 65 70 75 80

40 Phe Cys Arg Asp Met Lys Lys Phe Gly Gly Pro Asn Lys Ile Arg Gln 85 90 95
Lys Cys Arg Leu Arg Gln Cys Gln Leu Arg Ala Arg Glu Ser Tyr Lys 100 105 110

45 Tyr Phe Pro Ser Ser Leu Ser Pro Val Thr Pro Ser Glu Ser Leu Pro 115 120 125

50 Arg Pro Arg Arg Pro Leu Pro Thr Gln Gln Gln Pro Gln Pro Ser Gln 130 135 140

Lys Leu Gly Arg Ile Arg Glu Asp Glu Gly Ala Val Ala Ser Ser Thr 145 150 155 160

55 Val Lys Glu Pro Pro Glu Ala Thr Ala Thr Pro Glu Pro Leu Ser Asp 165 170 175

Glu Asp Leu Pro Leu

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<212> DNA
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<223> Description of artificial sequence: Primer
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